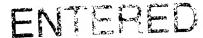PCT09

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PATENT APPLICATION: US/09/889,592   TIME: 15.56.34

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    7 <110> APPLICANT: Ingvar M. Ferby et al.
   13 <120> TITLE OF INVENTION: PROTEIN WITH CELL PROLIFERATION AND CELL DIVISION
   14       MODULATING ACTIVITY AND DNA ENCODING SUCH PROTEIN
   20 <130> FILE REFERENCE: 100561-00064
   26 <140> CURRENT APPLICATION NUMBER: 09/889,592
C--> 29 <141> CURRENT FILING DATE: 2001-10-31
   35 <150> PRIOR APPLICATION NUMBER: PCT/EP00/00877
   38 <151> PRIOR FILING DATE: 2000-02-03
   44 <150> PRIOR APPLICATION NUMBER: EP 99102172.6
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   59 <170> SOFTWARE: Patent-In version 3.1
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  106 tttatcgcca tttggccagt ggtggctaag cgcctgaagg tggctgcttc ctttgctcag     180
  110 atcaaccctc gggccggtgt ccccctttct aca atg agg cac atg cag agt gta     234
  112                                         Met Arg His Met Gln Ser Val
  114                                          1               5
  118 acc cgg gcc agc tcc att tgt ggc agc ggg gtg aag cag gtc att ggc     282
  120 Thr Arg Ala Ser Ser Ile Cys Gly Ser Gly Val Lys Gln Val Ile Gly
  122        10              15                  20
  126 aag ggg cat ccg cac gcc cgg gtt gtt gga gcg cgc aag gcg caa atc     330
  128 Lys Gly His Pro His Ala Arg Val Val Gly Ala Arg Lys Ala Gln Ile
  130        25              30                  35
  134 cct gag aga gag gag ttg tca gtc aaa ccc aaa atg gtg cga aat acc     378
  136 Pro Glu Arg Glu Glu Leu Ser Val Lys Pro Lys Met Val Arg Asn Thr
  138 40              45                  50                  55
  142 cat ctc aat cta cag ccc cag gag cgc cag gcc ttc tac agg ctc cta     426
  144 His Leu Asn Leu Gln Pro Gln Glu Arg Gln Ala Phe Tyr Arg Leu Leu
  146            60                  65                  70
  150 gaa aat gag cag att cag gaa ttc ctt tct atg gac tcc tgt cta agg     474
  152 Glu Asn Glu Gln Ile Gln Glu Phe Leu Ser Met Asp Ser Cys Leu Arg
  154            75                  80                  85
  158 att tcc gac aag tat ctc ata gca atg gtt cta gca tat ttt aag cgg     522
  160 Ile Ser Asp Lys Tyr Leu Ile Ala Met Val Leu Ala Tyr Phe Lys Arg
  162            90                  95                  100
  166 gca gcg ggc ctc tac acc agc gag tac aca acc atg aat ttc ttt gtt     570
  168 Ala Ala Gly Leu Tyr Thr Ser Glu Tyr Thr Thr Met Asn Phe Phe Val
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PATENT APPLICATION: US/09/889,592   TIME: 15:56:34

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170      105                    110                    115
174 gcc ctg tat ctg gct aat gac atg gag gaa gat gaa gaa gac tat aaa       618
176 Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu Asp Glu Glu Asp Tyr Lys
178 120                    125                    130                    135
182 tat gaa atc ttc ccc tgg gca cta gga gac tcg tgg cgt gag ctt ttc       666
184 Tyr Glu Ile Phe Pro Trp Ala Leu Gly Asp Ser Trp Arg Glu Leu Phe
186                     140                    145                    150
190 cca caa ttt ttg cgt ctc cgg gac gac ttc tgg gct aaa atg aac tac       714
192 Pro Gln Phe Leu Arg Leu Arg Asp Asp Phe Trp Ala Lys Met Asn Tyr
194                     155                    160                    165
198 cga gca gtt gtt agt cga agg tgc tgt gat gag gta atg tcc aaa gat       762
200 Arg Ala Val Val Ser Arg Arg Cys Cys Asp Glu Val Met Ser Lys Asp
202               170                    175                    180
206 ccc act cat tgg gcc tgg ctg aga gat cgc ccc atg cat cac agc ggg       810
208 Pro Thr His Trp Ala Trp Leu Arg Asp Arg Pro Met His His Ser Gly
210           185                    190                    195
214 gcc atg cgt ggt tac ctt aga aac gag gac gac ttt ttc ccc cgg ggt       858
216 Ala Met Arg Gly Tyr Leu Arg Asn Glu Asp Asp Phe Phe Pro Arg Gly
218 200                    205                    210                    215
222 cca ggc ctt aca cca gcc agc tgt aca ctt tac cat aaa gca ggt gtc       906
224 Pro Gly Leu Thr Pro Ala Ser Cys Thr Leu Cys His Lys Ala Gly Val
226           220                    225                    230
228 tgt gac tct ggt ggt gtc tcc cac aac aac tct tcc tct cca gaa caa       954
232 Cys Asp Ser Gly Gly Val Ser His Asn Asn Ser Ser Ser Pro Glu Gln
234               235                    240                    245
238 gag att ttt cac tac acc aat agg gag tgg tcc cag gag ctt ctc atg       1002
240 Glu Ile Phe His Tyr Thr Asn Arg Glu Trp Ser Gln Glu Leu Leu Met
242           250                    255                    260
246 ttg ccc cct gag ctg ttg ctg gat ccc gag tgt act cat gac tta cac       1050
248 Leu Pro Pro Glu Leu Leu Leu Asp Pro Glu Cys Thr His Asp Leu His
250           265                    270                    275
254 att ctc cag gag cca ttg gtt gga tta gag cca gat ggg acg gcg ctg       1098
256 Ile Leu Gln Glu Pro Leu Val Gly Leu Glu Pro Asp Gly Thr Ala Leu
258 280                    285                    290                    295
262 gaa tgg cac cac ctt tagtagccga ttgtctcctc cgagctttta ttcttctcta       1153
264 Glu Trp His His Leu
266                     300
270 ctcacaaget cagcacttat tctctcctcc taaggacttg tcaatgttca gacttaatta     1213
274 aaatggaga agtgaatatt ccgacggatg tagagcggga atatgtgccc agagaaagtg     1273
278 ttttgagtct gtataaaccg ttgctttgta aataaatata taaatgttct ctgtgctggt     1333
282 cactaataaa gatcagctaa aatcactttc aggtgtaatt taatagtatg tatgtagagt     1393
286 ctttaattca gctctccacc aaatagtaac ttgtcatcac tgaacctttg cttaactaca     1453
290 attttatttt tctgcacaca aatattctga agatcagacc gttctgtttt cagatggtt      1513
294 gaaaatatta aactcaacag aattcctgtg gtgtaatgta aatgcaaaga tcgattagac     1573
298 ta                                                                    1575
304 <210> SEQ ID NO: 2
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310 <212> TYPE: PRT
313 <213> ORGANISM: Xenopus sp
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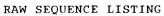PATENT APPLICATION   US/09/889,592   TIME: 15:56:34

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331 Gly Val Lys Gln Val Ile Gly Lys Gly His Pro His Ala Arg Val Val
333             20                  25                  30
339 Gly Ala Arg Lys Ala Gln Ile Pro Glu Arg Glu Glu Leu Ser Val Lys
341         35                  40                  45
347 Pro Lys Met Val Arg Asn Thr His Leu Asn Leu Gln Pro Gln Glu Arg
349     50                  55                  60
355 Gln Ala Phe Tyr Arg Leu Leu Glu Asn Glu Gln Ile Gln Glu Phe Leu
357 65                  70                  75                  80
363 Ser Met Asp Ser Cys Leu Arg Ile Ser Asp Lys Tyr Leu Ile Ala Met
365                 85                  90                  95
371 Val Leu Ala Tyr Phe Lys Arg Ala Ala Gly Leu Tyr Thr Ser Glu Tyr
373             100                 105                 110
379 Thr Thr Met Asn Phe Phe Val Ala Leu Tyr Leu Ala Asn Asp Met Glu
381         115                 120                 125
387 Glu Asp Glu Glu Asp Tyr Lys Tyr Glu Ile Phe Pro Trp Ala Leu Gly
389     130                 135                 140
395 Asp Ser Trp Arg Glu Leu Phe Pro Gln Phe Leu Arg Leu Arg Asp Asp
397 145                 150                 155                 160
403 Phe Trp Ala Lys Met Asn Tyr Arg Ala Val Val Ser Arg Arg Cys Cys
405                 165                 170                 175
411 Asp Glu Val Met Ser Lys Asp Pro Thr His Trp Ala Trp Leu Arg Asp
413             180                 185                 190
419 Arg Pro Met His His Ser Gly Ala Met Arg Gly Tyr Leu Arg Asn Glu
421         195                 200                 205
427 Asp Asp Phe Phe Pro Arg Gly Pro Gly Leu Thr Pro Ala Ser Cys Thr
429     210                 215                 220
435 Leu Cys His Lys Ala Gly Val Cys Asp Ser Gly Gly Val Ser His Asn
437 225                 230                 235                 240
443 Asn Ser Ser Ser Pro Glu Gln Glu Ile Phe His Tyr Thr Asn Arg Glu
445                 245                 250                 255
451 Trp Ser Gln Glu Leu Leu Met Leu Pro Pro Glu Leu Leu Leu Asp Pro
453             260                 265                 270
459 Glu Cys Thr His Asp Leu His Ile Leu Gln Glu Pro Leu Val Gly Leu
461         275                 280                 285
467 Glu Pro Asp Gly Thr Ala Leu Glu Trp His His Leu
469     290                 295                 300
477 <210> SEQ ID NO: 3
480 <211> LENGTH  1357
483 <212> TYPE: DNA
486 <213> ORGANISM: Xenopus sp.
492 <220> FEATURE:
495 <221> NAME/KEY: CDS
498 <222> LOCATION: (163)..(1056)
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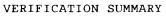PATENT APPLICATION: US/09/889,592

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514 ttcctgttca tcaccattct ttggccgttg gtggctaggc gcctgaaggt ggctgctacc    120
518 tttgctcaga tcaaccctcg gttcgttgtc cccctttcta ca atg agg cat atg        174
520                                                      Met Arg His Met
522                                                       1
526 cag agt gca acc cgg gcc acc tta gtt tgt ggc agc ggg gta aag cag        222
528 Gln Ser Ala Thr Arg Ala Thr Leu Val Cys Gly Ser Gly Val Lys Gln
530  5                   10                  15                  20
534 atc att gcc aag gga cat ccg aat acc cgg gtt ttt gga gcg cgc aag        270
536 Ile Ile Ala Lys Gly His Pro Asn Thr Arg Val Phe Gly Ala Arg Lys
538              25                  30                  35
542 gcg aaa atc cct gag aga gag gtg cta gca gcc aaa ccc aag atc acg        318
544 Ala Lys Ile Pro Glu Arg Glu Val Leu Ala Ala Lys Pro Lys Ile Thr
546              40                  45                  50
550 cgc att aca cat ctc aat cta caa ccc cag gag cgc cag gcc ttt tac        366
552 Arg Ile Thr His Leu Asn Leu Gln Pro Gln Glu Arg Gln Ala Phe Tyr
554          55                  60                  65
558 agg ctc cta gaa aat gag ctg att cag gaa ttt ctt tct atg gac tcc        414
560 Arg Leu Leu Glu Asn Glu Leu Ile Gln Glu Phe Leu Ser Met Asp Ser
562      70                  75                  80
566 tgt cta aag att tca gac aag tat ctc ata gca atg gtt cta gca tat        462
568 Cys Leu Lys Ile Ser Asp Lys Tyr Leu Ile Ala Met Val Leu Ala Tyr
570 85                  90                  95                  100
574 ttt aag agg gct ggt cta tac acc agt gag tat aca acc atg aat ttc        510
576 Phe Lys Arg Ala Gly Leu Tyr Thr Ser Glu Tyr Thr Thr Met Asn Phe
578                  105                 110                 115
582 ttt gtt gct ctg tat ctg gct aat gac atg gag gaa gat gaa gaa gac        558
584 Phe Val Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu Asp Glu Glu Asp
586              120                 125                 130
590 tat aaa tat gaa atc ttc ccc tgg gca cta gga gat tca tgg cgt gag        606
592 Tyr Lys Tyr Glu Ile Phe Pro Trp Ala Leu Gly Asp Ser Trp Arg Glu
594              135                 140                 145
598 ttt ttc cca caa ttt tta cgt ctc cgg gac gac ttc tgg gct aaa atg        654
600 Phe Phe Pro Gln Phe Leu Arg Leu Arg Asp Asp Phe Trp Ala Lys Met
602      150                 155                 160
606 aac tac cga gca gtt gtt agc cga aga tgt tgt gat gag gta atg gcg        702
608 Asn Tyr Arg Ala Val Val Ser Arg Arg Cys Cys Asp Glu Val Met Ala
610 165                 170                 175                 180
614 aaa gat ccc act cat tgg gcc tgg ctc aga gat cgt cct att cat cat        750
616 Lys Asp Pro Thr His Trp Ala Trp Leu Arg Asp Arg Pro Ile His His
618                  185                 190                 195
622 agt ggg gcc ctg cgt ggt tac ctc aga aat gag gat gac ttt ttc cct        798
624 Ser Gly Ala Leu Arg Gly Tyr Leu Arg Asn Glu Asp Asp Phe Phe Pro
626              200                 205                 210
630 cgg ggt cca ggc ctt aca cca gcc agc tgt gca ctt tgc cat aaa gca        846
632 Arg Gly Pro Gly Leu Thr Pro Ala Ser Cys Ala Leu Cys His Lys Ala
634              215                 220                 225
638 agt gtc tgt gac tct ggt ggg gtg tcc cat gac aac tct tct cca gaa        894
640 Ser Val Cys Asp Ser Gly Gly Val Ser His Asp Asn Ser Ser Pro Glu
642              230                 235                 240
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616  caa gag att ttt cac tac acc aat agg gag tgg tcc cag gaa ctt ctc    942
613  Gln Glu Ile Phe His Tyr Thr Asn Arg Gln Trp Ser Gln Glu Leu Leu
650  245              250              255              260
654  atc ttg cca cct gaa ctg tta ttg gat ccg gag tct act tat gac atc    990
656  Ile Leu Pro Pro Glu Leu Leu Leu Asp Pro Glu Ser Thr Tyr Asp Ile
658              265              270              275
662  cac att ttc cag gaa ccg ttg gtt gga tta gag cca gat gag gca gcc   1038
661  His Ile Phe Gln Glu Pro Leu Val Gly Leu Glu Pro Asp Gly Ala Ala
666              280              285              290
670  ttg gaa tgg cac cac ctt tagcaccatg tcatctctgt gctttcattc          1086
672  Leu Glu Trp His His Leu
674              295
678  ttctctaatc cacgagctca agaagcactt aacctctcct aagcacttgc ccatgtccct  1146
682  attcagacta atgaattaaa tgggagaggt gactattg c ataaagggaa ggatgccact  1206
686  tagagtggag aataatactt gccaaaaatg gtgtttgggt ctgtttaaac tgttgctatt  1266
690  tcagttgcct tgtaaataaa gaagtataaa gtgtatgct gtgccggt tgctaataaa  1326
694  aaaaaaatct ggtatcaaaa aaaaaaaaa a                                 1357
700  <210> SEQ ID NO: 4
702  <211> LENGTH: 298
705  <212> TYPE: PRT
708  <213> ORGANISM: Xenopus sp.
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726              20               25               30
732  Gly Ala Arg Lys Ala Lys Ile Pro Glu Arg Glu Val Leu Ala Ala Lys
734              35               40               45
740  Pro Lys Ile Thr Arg Ile Thr His Leu Asn Leu Gln Pro Gln Glu Arg
742         50               55               60
748  Gln Ala Phe Tyr Arg Leu Leu Glu Asn Glu Leu Ile Gln Glu Phe Leu
750  65                   70               75               80
756  Ser Met Asp Ser Cys Leu Lys Ile Ser Asp Lys Tyr Leu Ile Ala Met
758              85               90               95
764  Val Leu Ala Tyr Phe Lys Arg Ala Gly Leu Tyr Thr Ser Glu Tyr Thr
766              100              105              110
772  Thr Met Asn Phe Phe Val Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu
774              115              120              125
780  Asp Glu Glu Asp Tyr Lys Tyr Glu Ile Phe Pro Trp Ala Leu Gly Asp
782         130              135              140
788  Ser Trp Arg Glu Phe Phe Pro Gln Phe Leu Arg Leu Arg Asp Asp Phe
790  145              150              155              160
796  Trp Ala Lys Met Asn Tyr Arg Ala Val Val Ser Arg Arg Cys Cys Asp
798              165              170              175
804  Glu Val Met Ala Lys Asp Pro Thr His Trp Ala Trp Leu Arg Asp Arg
806              180              185              190
812  Pro Ile His His Ser Gly Ala Leu Arg Gly Tyr Leu Arg Asn Glu Asp
814              195              200              205
820  Asp Phe Phe Pro Arg Gly Pro Gly Leu Thr Pro Ala Ser Cys Ala Leu
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VERIFICATION SUMMARY
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L:29 M:271 C: Current Filing Date differs, Replaced Current Filing Date